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Connectedness in Targhee and Suffolk flocks participating in the United States National Sheep Improvement Program

L. A. Kuehn
Virginia Polytechnic Institute and State University, Larry.Kuehn@ars.usda.gov

R. M. Lewis
Virginia Polytechnic Institute and State University, ron.lewis@unl.edu

D. R. Notter
Virginia Polytechnic Institute and State University

Connectedness in Targhee and Suffolk flocks participating in the United States National Sheep Improvement Program[1]

L. A. Kuehn,[2,3] R. M. Lewis, and D. R. Notter

Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg 24061

ABSTRACT: Connectedness among animals in separate flocks reduces the risk of biased comparisons when selecting across flocks on EBV. The objective in this study was to assess levels of connectedness in the genetic evaluation of weaning weight among Targhee and Suffolk flocks participating in the US National Sheep Improvement Program (NSIP). Among flocks currently participating in the NSIP, a total of 25,404 weaning weight and 35,794 pedigree records were available for 16 Targhee flocks, and 14,017 weaning weight and 18,311 pedigree records were available for 24 Suffolk flocks. Connectedness was measured by using 2 different methods. First, numbers of progeny with recorded weaning weights from linking sires (defined as sires with progeny in multiple flocks or sires born in one flock with progeny in another flock) were counted. Second, connectedness was measured by calculating the average prediction error correlation of mean flock EBV (flock r_{ij}). Benchmarks for flock r_{ij} were established, with 0.10 and 0.05 representing low and moderate risk of bias associated with comparing EBV among flocks, respectively. From 1995 through 2004, 44% of Targhee lambs with weaning weights were born to linking sires; in Suffolk lambs, that value was 23%. In 1990, 1995, and 2005, average flock r_{ij} were 0.10, 0.19, and 0.28, respectively, among Targhee flocks, and 0.02, 0.02, and 0.04, respectively, among Suffolk flocks that participated in NSIP in all 3 yr. Among all active flocks in 2005, flock r_{ij} averaged 0.13 in Targhees and 0.03 in Suffolks. Hierarchical clustering of flocks based on flock r_{ij} revealed that all active Targhee flocks connected at a level near or above 0.10. In Suffolk flocks, 2 distinct clusters had formed, in which connectedness was relatively high within each cluster (flock r_{ij} near 0.10) but was near zero between clusters. Risk of bias in comparing EBV among flocks in the Targhee was low; however, caution should be exercised when comparing EBV between Suffolk flocks from different clusters.

Key words: connectedness, genetic evaluation, prediction error, sheep

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INTRODUCTION

Genetic evaluation in the US sheep industry is available to individual producers through the National Sheep Improvement Program (**NSIP**; Notter, 1998). Through the NSIP, BLUP EPD are predicted for a variety of traits for animals in participating flocks. Producers can use these EPD to make selection decisions within and across flocks. However, comparisons of animals across flocks may be biased if base animals in different flocks have different genetic means (Lewis et al., 1999) and if connectedness among flocks is insufficient (Kuehn et al., 2008a).

Genetic means can differ among populations because of genetic drift or selection (Falconer and MacKay, 1996). If either drift or selection occurs before the collection of pedigree and performance information, differences in flock genetic means may not be properly accounted for in the genetic evaluation model until sufficient connectedness has been achieved (Hanocq et al., 1996; Kuehn et al., 2008a).

In the United States, genetic differences among sheep flocks are likely. For many sheep breeds, flocks are spread over a wide geographical region. Flocks sizes are generally small relative to other livestock species, and AI use, an effective tool for connecting herds of beef and dairy cattle, is practically nonexistent in sheep (National Animal Health Monitoring System, 2001). In contrast to other countries such as the United Kingdom, cooperative breeding schemes, designed to create such genetic links (Lewis and Simm, 2000), have rarely

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[2]Corresponding author: larry.kuehn@ars.usda.gov
[3]Current address: USDA-ARS, US Meat Animal Research Center, Clay Center, NE 68933.

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Table 1. Summary of pedigree and weaning performance data for the Targhee and Suffolk breeds participating in the National Sheep Improvement Program

	Targhee		Suffolk	
Item	All flocks	Active flocks[1]	All flocks	Active flocks[1]
No. of inventoried animals	41,894	35,794	36,239	18,311
No. of sires	934	661	2,525	1,233
No. of dams	11,933	9,627	11,370	5,185
No. of sires with progeny weaning weights	429	350	1,235	640
No. of flocks	41	16	83	24
No. of weaning weight records	27,464	25,404	26,165	14,017
No. of contemporary groups	405	320	2,451	1,322
Average contemporary group size	67.8	79.4	10.7	10.6
Median contemporary group size	27.0	40.5	5.0	5.0
Average no. of sires per contemporary group	3.0	3.3	2.0	2.1

[1]Active flocks were those that reported data for lambs born in 2004 in Targhee and 2005 for Suffolk.

been used in the United States. An assessment of connectedness among US sheep flocks that participate in the NSIP would allow determination of the risk of bias when comparing and selecting animals from different flocks on EPD (Kuehn et al., 2008b). The objectives of this study were to assess the current amount of risk of bias in comparing EPD across Targhee or Suffolk flocks participating in the NSIP and to recommend future breeding strategies designed to manage this risk.

MATERIALS AND METHODS

Data for this study were taken from existing databases; therefore, Institutional Animal Care and Use Committee approval was not needed.

Data

The US NSIP was initiated in 1987 to provide genetic evaluations for the US sheep industry (Wilson and Morrical, 1991). Producers (rather than breed associations) submit pedigree and performance data to a central processing center and receive EPD for their active animals. Initially, traits were analyzed by using within-flock, single-trait models (Notter, 1998), but in 1994, multiple-trait, across-flock analyses began for the Targhee breed. Similar approaches were implemented for the Suffolk and Polypay in 1995 and 1996, respectively. In 2005, across-flock BLUP EPD were produced for 9 different sheep breeds. Of these breeds, several Targhee and Suffolk flocks had participated in NSIP since its inception. The perceived extent of connectedness and quantity of data were greatest for these breeds, and they were selected to evaluate changes in connectedness over time and current levels of connectedness.

In the Targhee, EPD are derived for 120-d weaning weight, yearling gain (120- to 365-d), fleece weight, fiber diameter, staple length, and percentage of lamb crop (number of lambs born per 100 ewes lambing), whereas Suffolk breeders receive EPD for 60-d weaning weight, 60- to 120-d postweaning gain, and percentage of lamb crop. Weaning weight and percentage of lamb crop are the only common traits evaluated in both breeds. For this study, connectedness in the genetic evaluation of weaning weight was evaluated in both breeds as a basis of comparison between the 2 data sets.

Valid weaning weights were defined as those recorded within 60-d windows (30 to 90 d for 60-d weaning weight in the Suffolk; 90 to 150 d for 120-d weaning weight in the Targhee). Weaning weights were excluded for animals without a reported dam age or type of birth and rearing, or if the lamb was fostered or artificially reared. Contemporary groups for weaning weight were formed based on flock, producer-supplied management codes, and weigh period (Notter, 1998). To be classified within the same weigh period, lambs had to be weighed in the same 7-d window. Management codes defined whether animals were or were not creep-fed and whether dams were fed alike or according to the number of lambs nursed. Producers also had the opportunity to augment management codes if lambs were treated differently for other reasons. Suffolk contemporary groups were further augmented by the age of animals at weaning; animals less than 40 d of age, 40 to 80 d of age, and greater than 80 d of age were placed in separate contemporary groups.

A summary of pedigree and performance data is presented in Table 1. Targhee flock sizes ranged from approximately 20 to 230 breeding ewes, with a median flock size of approximately 65 ewes. Targhee flocks tended to be found in the western United States, with only 8 states represented in the data. Currently active Targhee flocks came from only 4 states; 13 of the 16 active flocks were from Montana. Weaning weight records were reported from 1984 through 2004. Targhee flocks began an active exchange of rams in 1994, about the time across-flock analysis began. Because of this policy, and the relatively close proximity of the flocks to one another, connectedness among Targhee flocks was expected to be substantial.

Suffolk flocks ranged in size from approximately 20 to 140 breeding ewes, with a median flock size of approximately 40 ewes, and flocks were spread widely across the United States, with 27 states represented. The currently active Suffolk flocks were located in 14 states. Weaning weights were reported from 1983 through

2005. The NSIP Suffolk flocks had never attempted a formal exchange of rams among flocks. Some amount of exchange is believed to have taken place through purchases of rams from prominent breeders and at national shows. However, many of the purchased rams did not come from NSIP flocks and therefore would not provide connections for genetic evaluation. Because of the wide distribution of flocks across the United States and the lack of an active exchange program, connectedness was expected to be more limited among Suffolk flocks.

Measuring Connectedness

In its 18-yr history, participation in the NSIP has been variable. Several flocks joined the NSIP at some point but no longer participated. Because connectedness is of greater relevance to the flocks that are currently active in the program, connectedness measures and counts were summarized only for active flocks.

Connectedness across flocks is established primarily through the use of common sires in different flocks and through the purchase of rams born in other NSIP member flocks. One way to map the establishment of connectedness is to count the number of progeny of such linking sires with recorded weaning weights. Sires were thus classified into 1 of 4 different categories: 1) sires used in multiple flocks; 2) sires used in a single flock but born in a different NSIP flock; 3) sires used in the NSIP flock in which they were born; and 4) non-NSIP sires used in a single flock. Sires used in multiple flocks included both sires born in NSIP flocks and those born in non-NSIP flocks. Sires used in the same NSIP flocks in which they were born do not contribute to connectedness among flocks. However, they are an important source of connectedness between contemporary groups within their flock and therefore allow linking sires to have a greater impact across different years. The number of progeny from each sire type was calculated for each of the 18 yr of pedigree and performance data recording. Origins of sires of lambs born before the NSIP was begun could not be definitively established.

Connectedness between flocks was quantified through the use of prediction error correlations (Lewis et al., 1999, 2005; Kuehn et al., 2008b), also known as connectedness correlations. Prediction errors were derived under the following linear animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of weaning weights, $\mathbf{b}$ is a vector of fixed effects, $\mathbf{u}$ is a vector of breeding values, and $\mathbf{e}$ is a vector of residuals. Incidence matrices $\mathbf{X}$ and $\mathbf{Z}$ relate phenotypes to fixed and random genetic effects, respectively. Only contemporary group was fitted as a fixed effect; adjustments for effects of age of dam, type of birth and rearing, and lamb age were applied before analysis of the data (Bradford, 2003). Prediction error (co)variances of EBV from this model were derived from the inverse of the coefficient matrix ($\mathbf{C}$) used to derive EBV:

$$\mathbf{C} = [\mathbf{Z}'\mathbf{M}\mathbf{Z} + \lambda\mathbf{A}^{-1}],$$

where $\mathbf{M}$ is the fixed effect absorption matrix $\left[\mathbf{M} = \mathbf{I} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-}\mathbf{X}'\right]$, λ is the ratio of residual and additive variances $\left(\sigma_e^2 / \sigma_a^2\right)$, and $\mathbf{A}$ is the numerator relationship matrix. Inverse elements of $\mathbf{C}$, multiplied by σ_e^2, are prediction error (co)variances of EBV. Prediction errors of breeding value predictions will be independent for pairs of animals evaluated in separate contemporary groups and lacking genetic connections (Kennedy and Trus, 1993). In contrast, pairs of animals evaluated in the same management units or connected through common pedigree ties will have a positive prediction error covariance. Thus, the connectedness correlation (flock r_{ij}) proposed by Lewis et al. (1999, 2005) was derived for flocks i and j as

$$r_{ij} = \frac{\mathrm{PEC}(\hat{\bar{u}}_{i.}, \hat{\bar{u}}_{j.})}{\sqrt{\mathrm{PEV}(\hat{\bar{u}}_{i.})\mathrm{PEV}(\hat{\bar{u}}_{j.})}},$$

where $\hat{\bar{u}}_{i.\ (j.)}$ is the mean EBV of all animals in flock $i(j)$, $\mathrm{PEC}(\hat{\bar{u}}_{i.}, \hat{\bar{u}}_{j.})$ is the prediction error covariance between these means, and $\mathrm{PEV}(\hat{\bar{u}}_{i.})$ and $\mathrm{PEV}(\hat{\bar{u}}_{j.})$ are the prediction error variances of the mean EBV of flocks i and j. Heritability estimates of 0.10 for Targhee and 0.15 for Suffolk (Notter, 1998) were used in the model to derive prediction error variances and covariances.

Using simulation, Kuehn et al. (2008b) established that flock r_{ij} can be used as a measure of the risk of bias when comparing EBV of animals across flocks. In that study, flocks were simulated with different genetic means to introduce partial bias in comparing animals across flocks. Connecting flocks through the use of different sire referencing schemes decreased the bias in comparisons of EBV of animals from different flocks. The decrease in bias had a strong relationship with flock r_{ij}; a flock r_{ij} of 0.05 corresponded to a reduction of approximately 80% in bias, and a flock r_{ij} of 0.10 corresponded to a reduction of approximately 90%. These benchmarks of 0.05 and 0.10 were proposed for use in monitoring risks of bias associated with comparing animals across flocks.

These benchmarks were based on scenarios using a heritability of 0.25 (Kuehn et al., 2008b). To validate that the same benchmark levels of flock r_{ij} were applicable to data with less heritability, 25 replicates of a continuous AI sire referencing scheme with selection on a trait with heritability of 0.125 were simulated over 15 yr by using the methods described in Kuehn et al. (2008a,b). Flock r_{ij} in each year of the program were plotted against the percentage reduction in bias (Figure 1). The relationship between bias and flock r_{ij}

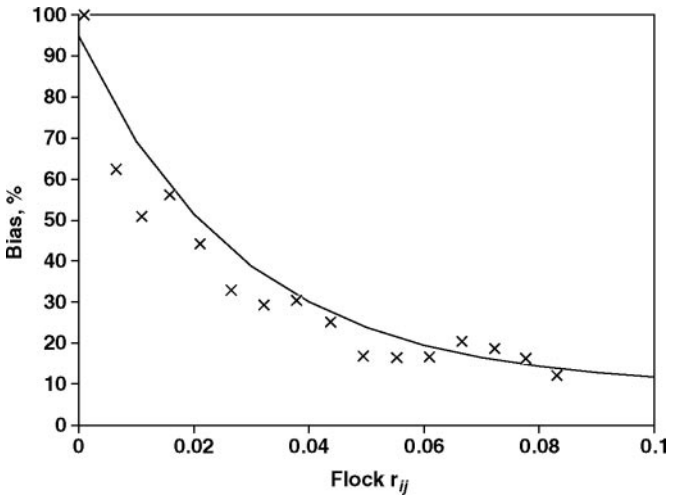

Figure 1. Relationships between the average percentage of bias remaining and flock connectedness correlation (flock r_{ij}) for 15 flocks participating in a sire referencing scheme over 15 yr of selection on a trait with a heritability of 0.125.

over time was essentially the same as that reported by Kuehn et al. (2008b). Therefore, benchmarks of 0.05 for "good" connectedness and 0.10 for "superior" connectedness were used to evaluate results obtained for Targhee and Suffolk flocks.

To examine how connectedness has changed, flock r_{ij} were calculated between pairs of currently active flocks at 3 different times: 1990, 1995, and the most recent year in which data were available (2004 for Targhee and 2005 for Suffolk). These years were chosen to reflect the state of connectedness shortly after the NSIP began (1990), during the year that across-flock evaluations began (1995), and currently. Data sets for 1990 and 1995 were created by removing pedigree and performance records of animals born after these years from the current databases. Pedigree and performance data from flocks that were not currently active in NSIP (flocks that had been members of the NSIP but discontinued participation before 2004 for Targhee and 2005 for Suffolk) were retained to allow for potential indirect connections. Of the 16 currently active Targhee flocks, 4 were participating in NSIP in 1990 and 10 were participating in 1995. In Suffolks, 6 of the currently active 24 flocks were members of the NSIP in 1990 and 9 were members in 1995. Flock r_{ij} was summarized for these active flocks relative to each of the 3 time points.

Using flock r_{ij} calculated from the most recent data, we performed hierarchical clustering of active flocks in each breed. Flock r_{ij} was used to measure the distance between flocks. Clustering was based on the group-average criterion. The similarity between 2 flocks or clusters of flocks was defined as the average distance between all pairs of units involving a member of each group. Groups merged with whichever groups were closest in average distance, and the average similarity of the resulting cluster with other groups was recalculated. The resulting links between flocks and clusters were plotted as dendrograms. The clustering results and dendrogram plots were obtained by using the CLUSTER and TREE procedures (SAS Inst. Inc., Cary, NC). We hypothesized that matings that would enhance connectedness across all flocks could be identified by examining the connected clusters formed within each of these breeds; exchange of sires from distinct clusters would likely tie the across-flock evaluation together.

RESULTS

Numbers of Progeny from Linking Sires

Figures 2 and 3 show the numbers of progeny produced by each type of sire in the Targhee and Suffolk breeds, respectively. In the last 5 yr, an average of 1,911 progeny weaning weights were recorded per year in the 16 Targhee flocks; an average of 1,202 weaning weights were recorded per year in the 24 Suffolk flocks. The number of animals with weaning weight records that were progeny of sires from non-NSIP flocks (used in a single flock) was relatively constant across years, but the average proportion of lambs from non-NSIP sires declined over time and was much less in Targhees (16%) than in Suffolks (39%).

When across-flock analysis began in Targhees in 1995, an increase in the number of weaning weights was recorded because of new (currently active) flocks joining the evaluation (Figure 2). As expected, the number of progeny from multiple-use sires, and the number of progeny born to sires that were transferred to other member flocks (i.e., single between), also began to increase at about this time. From 1995 through 2004, 44% of the Targhee lambs with weaning weight records were born from sires that were either transferred to a different flock or used in multiple flocks.

The number of Suffolk weaning weight records increased relatively little in the years immediately after introduction of the across-flock analyses in 1995. The number of weaning weights recorded in the Suffolk breed in these intermediate years was greater than that shown in Figure 3; however, a large number of flocks discontinued their membership in NSIP (Table 1) and thus their data were not included. The numbers of weaning records have steadily increased in the last 5 yr, however, primarily because new flocks began to enroll after 1999. As mentioned previously, only 9 of the currently active flocks participated in the NSIP in 1995. Since then, 13 new flocks have enrolled, bringing the total number of active flocks to 24. In the last 10 yr, 23% of the animals with weaning weight records were from sires used in multiple flocks or sires transferred to other member NSIP flocks, and the use of transferred sires has grown over the past 5 yr.

Connectedness Correlations

The mean, median, and SD of flock r_{ij} for groups of active Targhee and Suffolk flocks are summarized in Tables 2 and 3. Across all years and groups of flocks,

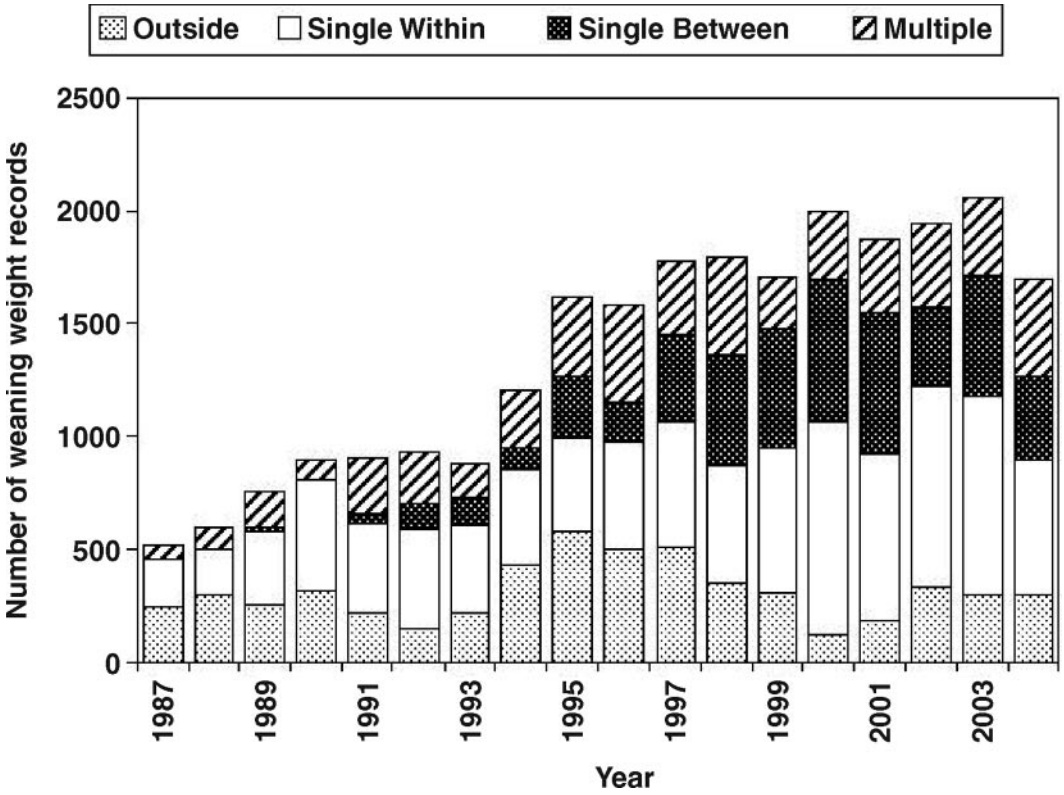

Figure 2. Numbers of Targhee lambs born from 1987 through 2004, with weaning weight records from sires originating outside the National Sheep Improvement Program (NSIP; Outside), sires used only in their flock of origin (Single Within), sires born in an NSIP flock but used only in a different NSIP flock (Single Between), and sires used in multiple NSIP flocks (Multiple).

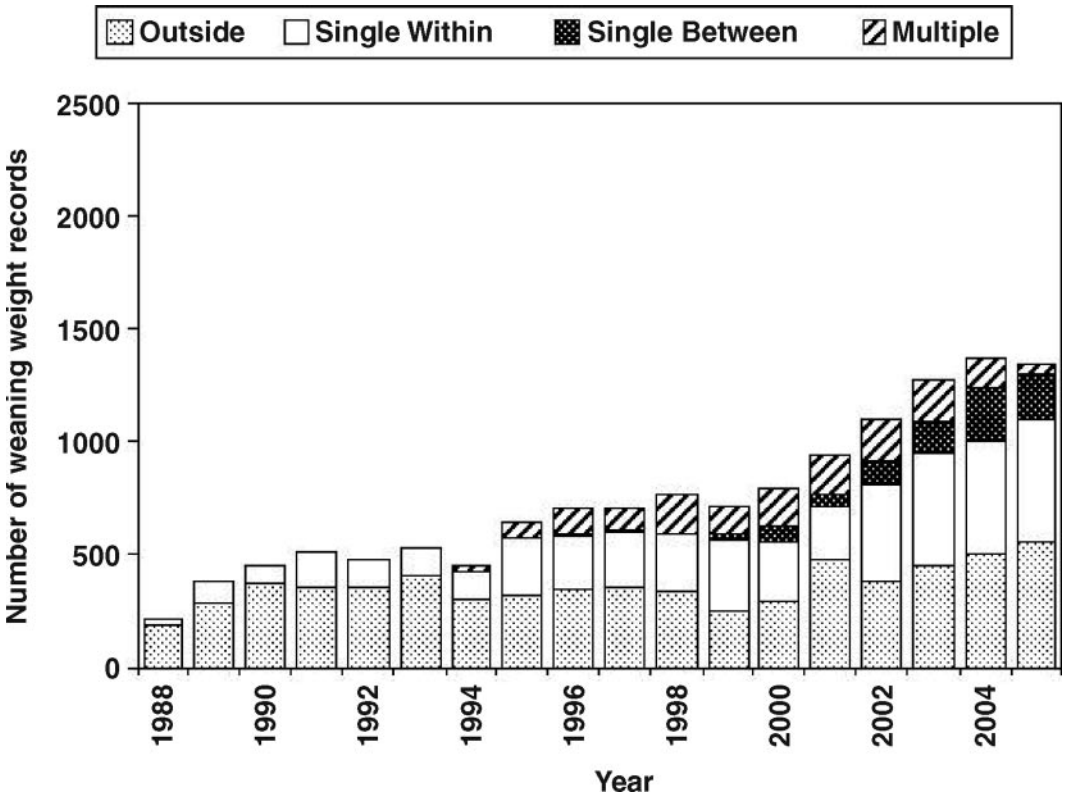

Figure 3. Numbers of Suffolk lambs born from 1988 through 2005, with weaning weight records from sires originating outside the National Sheep Improvement Program (NSIP; Outside), sires used only in their flock of origin (Single Within), sires born in an NSIP flock but used only in a different NSIP flock (Single Between), and sires used in multiple NSIP flocks (Multiple).

Table 2. In Targhee, descriptive statistics for the connectedness correlations (flock r_{ij}) as evaluated among currently active flocks recording in the National Sheep Improvement Program since 1990, 1995, and 2004

Year of evaluation	1990 (4)[1]		1995 (10)[1]		2004 (16)[1]	
	Mean (SD)	Median	Mean (SD)	Median	Mean (SD)	Median
1990	0.10 (0.075)	0.09				
1995	0.19 (0.055)	0.18	0.08 (0.072)	0.04		
2004	0.28 (0.049)	0.28	0.18 (0.092)	0.19	0.13 (0.110)	0.11

[1]Numbers of flocks recording for that year.

connectedness was much greater in the Targhee breed than in the Suffolk breed. Targhee flocks that had actively participated in NSIP since at least 1990 achieved average flock r_{ij} levels of 0.28 in 2004. Across all active Targhee flocks, mean flock r_{ij} in 2004 was above the greater benchmark level of 0.10. The mean and median flock r_{ij} were generally similar in the Targhee, suggesting that the values of flock r_{ij} were not heavily skewed in either direction.

Suffolk connectedness did not increase between 1990 and 1994 for the 6 flocks active during the early period as well as currently. Even by 2005, the mean level of flock r_{ij} in these 6 flocks was only 0.04. In all cases, the median value of flock r_{ij} was less than the mean value; this right-skewed distribution was because the flock r_{ij} value was near zero for many pairs of flocks. In 2005, more than 25% of all pairwise flock r_{ij} values were less than 0.002. However, in contrast, in another 25% of the cases these values were more than 0.04, causing the mean to increase relative to the median. These disparate flock r_{ij} values suggest that Suffolk flocks may be connecting primarily within smaller clusters rather than across the whole breed.

A dendrogram based on the group-average criterion for Targhee flocks that are currently active is presented in Figure 4. Flocks 1 through 4 had joined the NSIP before 1990, and flocks 5 through 10 had joined between 1990 and 1995. Two separate pairs of flocks were very closely connected: flocks 9 and 13 had a flock r_{ij} of 0.69, and flocks 2 and 15 had a flock r_{ij} of 0.53. In both cases, the rams used in 1 of the flocks came almost exclusively from the other flock (flock 13 from flock 9 and flock 15 from flock 2). All Targhee flocks merged into clusters at flock r_{ij} values greater than 0.05, the good connectedness benchmark. Flocks 1, 2, 3, 4, 9, 13, and 15 all merged into 1 cluster, with an average flock r_{ij} above 0.20. Only 2 flocks (10 and 14) did not merge with the main cluster at a flock r_{ij} level of 0.10 or above, the superior connectedness benchmark.

Clusters formed and merged at decreased levels of flock r_{ij} in the Suffolk breed (Figure 5). Flocks 1 through 6 are the active flocks that began the NSIP before 1990. Flocks 7, 8, and 9 joined the NSIP by 1995, and the remaining flocks (10 through 24) joined between 1995 and 2005. As seen in the dendrogram, 5 pairs of flocks had a pairwise flock r_{ij} of 0.20 or greater. Four clusters of flocks were formed at a threshold flock r_{ij} of 0.05 or greater. Cluster A consisted of flocks 1 and 9; cluster B contained flocks 2, 3, 11, 12, 13, 14, 15, 18, and 22; cluster C contained flocks 4, 5, 7, 20, 23, and 24; and cluster D consisted of flocks 16 and 17. Several other flocks were isolated from these larger clusters (e.g., flock 19). Cluster D, containing flocks 16 and 17, and flock 19 were basically unconnected from all the other flocks. The 2 large clusters (B and C) both contained several flocks that had participated in the NSIP for more than 10 yr. From these results, and those shown in Table 3, it appears there has been little incentive for some flocks that are long-term participants in the NSIP to connect with one another.

DISCUSSION

Connectedness in genetic evaluation is important if management units (e.g., flocks or herds) differ in their genetic mean. By increasing connectedness, the risk of biased EBV comparisons among units is reduced (Kennedy, 1981). Reduced selection bias and increased genetic diversity resulting from connecting units has been shown to increase genetic gains in simulated designed

Table 3. In Suffolks, descriptive statistics for the connectedness correlations (flock r_{ij}) as evaluated among currently active flocks recording in the National Sheep Improvement Program since 1990, 1995, and 2005

Year of evaluation	1990 (6)[1]		1995 (9)[1]		2005 (24)[1]	
	Mean (SD)	Median	Mean (SD)	Median	Mean (SD)	Median
1990	0.02 (0.041)	<0.01				
1995	0.02 (0.025)	0.01	0.01 (0.024)	<0.01		
2005	0.04 (0.040)	0.02	0.04 (0.049)	0.02	0.03 (0.051)	0.01

[1]Numbers of flocks recording for that year.

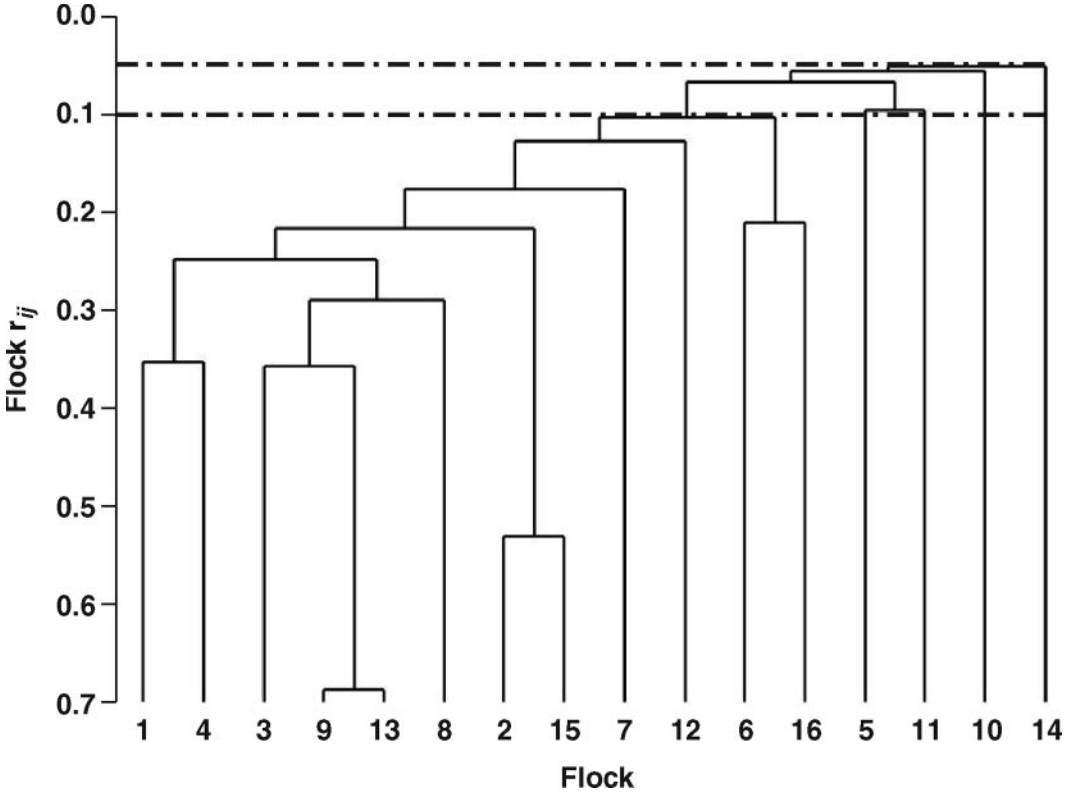

Figure 4. Cluster analysis of active National Sheep Improvement Program Targhee flocks in which groups are merged at their average distance (flock r_{ij}). Dashed lines indicate levels for "good" ($r_{ij} = 0.05$) and "superior" ($r_{ij} = 0.10$) connectedness.

breeding plans (Hanocq et al., 1996; Lewis and Simm, 2000; Kuehn et al., 2008a). Therefore, a measure of the level of connectedness would allow producers to monitor the risk of comparing their animals with those in other management units. Most measures developed to evaluate connectedness have been functions of prediction error (co)variances (e.g., Kennedy and Trus, 1993; Laloë 1993; Mathur et al., 2002), as was flock r_{ij} in this study. These statistics have been used to measure connectedness in dairy cattle (Hanocq and Boichard, 1999), swine (Hofer, 1994; Bunter and Macbeth, 1997; Mathur et al., 2002), and beef cattle (Roso et al., 2004). In general, these studies either have shown that connectedness was sufficient in the population of interest (e.g., dairy cattle; Hanocq and Boichard, 1999) or have revealed outlying management units (e.g., herds) that need to improve connections to increase the accuracy of comparisons with animals in other management units (e.g., swine; Hofer, 1994). Currently, connectedness evaluations are routinely conducted in Canada for swine by using the correlation between the SE of estimated herd effects (Mathur et al., 2002) and in sheep flocks in the United Kingdom by using flock r_{ij} (Simm et al., 2001). Producers are able to make future mating decisions based on their existing and desired level of connectedness to other herds or flocks. Using the results of this study, Targhee and Suffolk sheep breeders will have a similar opportunity.

Based on both numbers of progeny of linking sires and connectedness levels summarized by flock r_{ij}, the Targhee breed has clearly emphasized the establishment and maintenance of connections to a larger extent than has the Suffolk breed. Use of the same sires in multiple flocks, and the purchase of rams from other NSIP member flocks, has been a priority for Targhee breeders. As a result, connectedness among NSIP Targhee flocks has grown over time, especially since across-flock genetic evaluations began in 1995. By 2004, some of the newer Targhee flocks in the NSIP were effectively satellite units of other flocks that had participated over many years. By using sires from well-connected NSIP flocks, these new flocks quickly became strongly connected with other Targhee flocks in the NSIP. New flocks entering the NSIP can therefore rapidly become connected to the entire breed by purchasing sires from flocks that are already well connected. None of the Targhee flocks had poor overall connectedness. However, flocks 10 and 14 could reduce their risk of bias when comparing the EPD of their animals with those in other NSIP flocks by increasing their use of sires originating from these flocks; this could be achieved most efficiently by choosing rams from the 4 Targhee flocks with the longest history of participation in the NSIP.

The overall use of linking sires in the Suffolk breed has been much less than in the Targhee breed, but has increased, especially after 1995. The clusters formed by using flock r_{ij} imply that many of the linkages that occurred were within distinct subsets of flocks. Connectedness was reasonable between flocks within these clusters, but generally was much poorer between the clusters. Even some of the flocks that participated in NSIP since before 1990 were not well connected. Com-

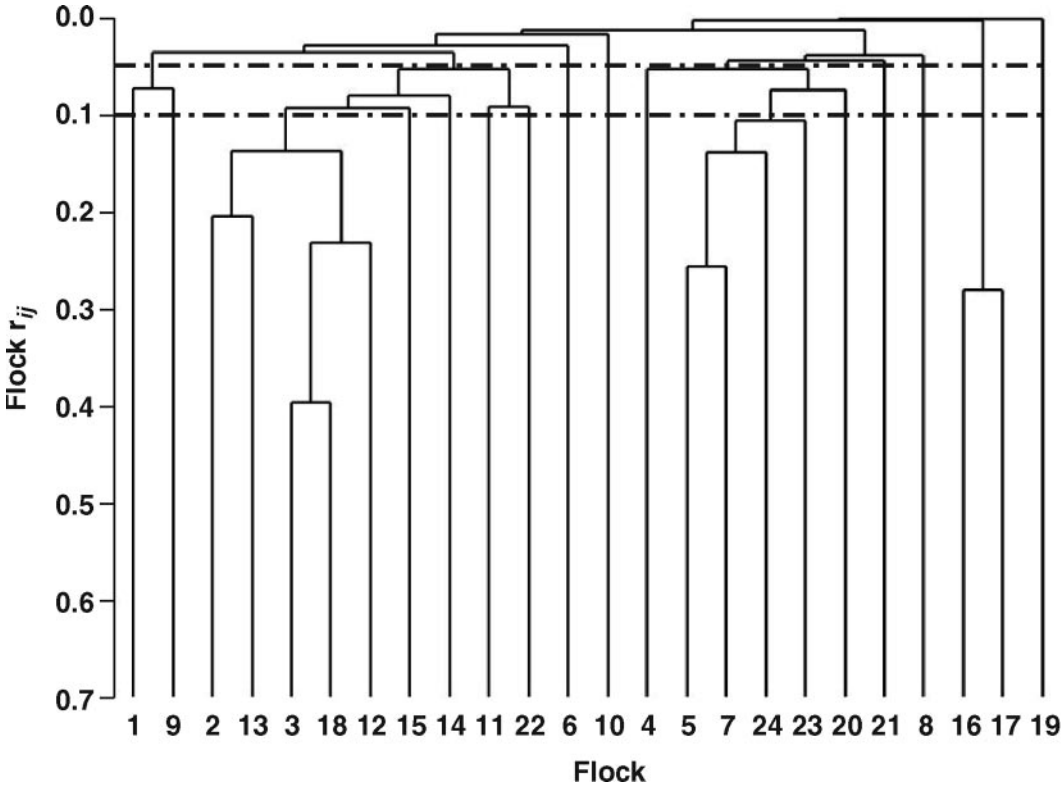

Figure 5. Cluster analysis of active National Sheep Improvement Program Suffolk flocks in which groups are merged at their average distance (flock r_{ij}). Dashed lines indicate levels for "good" ($r_{ij} = 0.05$) and "superior" ($r_{ij} = 0.10$) connectedness.

parisons of EPD across these clusters may therefore be more susceptible to biases.

Differences in connectedness levels between the breeds mainly seem to be due to different patterns of ram exchange: between all flocks in the Targhee vs. within clusters or subsets of flocks in the Suffolk. This situation likely reflects their structural features. The Targhee is a western range breed, with flocks primarily located within the same region; all but 3 of the flocks in this analysis were located in Montana. Because almost all the matings in the US sheep industry are by natural service, the close proximity of these flocks has made ram exchange more feasible. Furthermore, despite being a dual-purpose breed raised for both wool and meat production, Targhee breeders participating in the NSIP have similar breeding objectives, creating the potential for many flocks to purchase and use related individuals.

Suffolk connections may have been more challenging to establish. Unlike the Targhee flocks, Suffolk flocks in this analysis were scattered across the United States. Suffolk breeders have not formed cooperative ram exchange programs, in part because of the physical distances between flocks. In addition, although the Suffolk had the greatest number of annual registrations of any US sheep breed (*The Banner Sheep Magazine*; March 2008 issue), the numbers of animals recorded in the NSIP have been considerably less than in the Targhee. Several Suffolk flocks that participated in the NSIP and contributed a large portion of the weaning weight data later discontinued their participation. Although there has been a resurgence in both flock and animal numbers in the last 5 yr, most Suffolk flocks are not currently enrolled in the NSIP. A large proportion of the rams used in NSIP Suffolk flocks came from nonrecording flocks, especially before 2000. Because the pedigrees of these animals are not reported and they are used in single flocks, they do not contribute to connectedness.

An additional characteristic of the Suffolk breed that likely affects connectedness is divergent selection toward 2 different biological types (S. P. Greiner, Virginia Tech, Blacksburg, personal communication), one selected primarily for traditional terminal sire characteristics such as large mature size, and another with greater emphasis on moderate mature size and evidence of muscling. Breeders with these separate priorities are unlikely to purchase rams from one another, which is consistent with the separation of flocks into the clusters. Both of the larger clusters contain flocks from similar geographical regions that have never formed connections with one another.

Further improvement of connectedness in the Targhee need not be a priority. As long as current practices continue, risks of bias when comparing animals across flocks in this breed should be of no concern. Although not quantified by measures considered in this study, the risk of bias when comparing animals across unconnected Targhee flocks is probably also less than in the Suffolk flocks. Because the Targhee breed was established relatively recently (Bromley et al., 2000), genetic means between Targhee flocks have had less time to diverge.

If Suffolk breeders or their commercial customers wish to compare animals across clusters of flocks, greater exchange of rams between the clusters is critical. However, if the producers in these clusters truly are selecting toward different types of Suffolk sheep, connectedness between clusters may be of little importance; animals will be selected only from the cluster that matches the breeding goals of the buyers. New flocks joining the NSIP and current members that are poorly connected generally should purchase animals from the cluster that fits their breeding objective. Additional recruitment of flocks into the NSIP that are influential to the breed as a whole could also improve connectedness by creating additional pedigree linkages between flocks. If groups of breeders wish to work toward a common goal, a cooperative ram exchange program would improve rates of genetic gain and connectedness between flocks (Kuehn et al., 2008a).

Connectedness levels for fleece traits in the Targhee and litter size in both breeds may reflect slightly different patterns between flocks relative to weaning weight. Flocks that participate in the NSIP are required to report weaning weights and litter sizes, so levels of connectedness derived for weaning weight records are likely reflective of levels of connectedness for litter size, although preferential retention of replacement ewes from different sires and the additional time required for expression of litter size records could result in decreased levels and less rapid increases in connectedness over time. Reporting of fleece data are optional in the NSIP. Of the 16 currently active Targhee flocks, only 9, 10, and 6 have consistently reported fleece weights, fiber diameters, and staple lengths, respectively, since 2003. These fleece traits had genetic correlations with weaning weight of only 0.49, 0.0, and 0.0, respectively. Thus, connectedness levels for fleece traits may be less than those observed for weaning weight.

Both the Targhee and Suffolk breeds have established genetic connections among flocks through participation in the NSIP. Connections in the Targhee are effective across the entire breed, whereas Suffolk connectedness is confined to subsets or clusters of flocks. Exchange of rams and purchase of rams from other flocks can effectively increase connectedness and reduce the risk of bias when EPD of animals from different flocks are compared. Flocks joining genetic evaluation programs such as the NSIP should purchase rams from members with established genetic links to other flocks within the breed.

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